

SEQUENCE LISTING

<110> Economides, Aris N.
 Stahl, Neil
 Valenzuela, David M.
 Yancopoulos, George D.

<120> Therapeutic Method For Treating Bone
 Formation Diseases

<130> REG 132B1-C

<140> to be assigned

<141> 2003-12-12

<150> 09/897,322

<151> 2001-07-02

<150> 08/392,935

<151> 1995-03-03

<150> PCT/US93/08326

<151> 1993-09-02

<150> 09/957,401

<151> 1992-10-06

<150> 07/950,410

<151> 1992-09-23

<150> 07/939,954

<151> 1992-09-03

<160> 10

<170> FastSEQ for Windows Version 4.0

<210> 1

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<212> DNA

<213> Homo sapien

<220>

<221> CDS

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gtc	ctg	ggg	ctg	cgg	gcg	aca	ccg	gcc	ggc	ggc	cag	cac	tat	ctc	cac	96
Val	Leu	Gly	Leu	Arg	Ala	Thr	Pro	Ala	Gly	Gly	Gln	His	Tyr	Leu	His	
			20					25				30				

atc	cgc	ccg	gca	ccc	agc	gac	aac	ctg	ccc	ctg	gtg	gac	ctc	atc	gaa	144
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Ile	Arg	Pro	Ala	Pro	Ser	Asp	Asn	Leu	Pro	Leu	Val	Asp	Leu	Ile	Glu		
		35					40					45					
cac	cca	gac	cct	atc	ttt	gac	ccc	aag	gaa	aag	gat	ctg	aac	gag	acg	192	
His	Pro	Asp	Pro	Ile	Phe	Asp	Pro	Lys	Glu	Lys	Asp	Leu	Asn	Glu	Thr		
	50					55					60						
ctg	ctg	cgc	tcg	ctg	ctc	ggg	ggc	cac	tac	gac	cca	ggc	ttc	atg	gcc	240	
Leu	Leu	Arg	Ser	Leu	Leu	Gly	Gly	His	Tyr	Asp	Pro	Gly	Phe	Met	Ala		
	65				70					75					80		
acc	tcg	ccc	ccc	gag	gac	cgg	ccc	ggc	ggg	ggc	ggg	ggt	gca	gct	ggg	288	
Thr	Ser	Pro	Pro	Glu	Asp	Arg	Pro	Gly	Gly	Gly	Gly	Gly	Ala	Ala	Gly		
				85				90						95			
ggc	gcg	gag	gac	ctg	gcg	gag	ctg	gac	cag	ctg	ctg	cgg	cag	cgg	ccg	336	
Gly	Ala	Glu	Asp	Leu	Ala	Glu	Leu	Asp	Gln	Leu	Leu	Arg	Gln	Arg	Pro		
			100					105					110				
tcg	ggg	gcc	atg	ccg	agc	gag	atc	aaa	ggg	cta	gag	ttc	tcc	gag	ggc	384	
Ser	Gly	Ala	Met	Pro	Ser	Glu	Ile	Lys	Gly	Leu	Glu	Phe	Ser	Glu	Gly		
	115						120					125					
ttg	gcc	cag	ggc	aag	aag	cag	cgc	cta	agc	aag	aag	ctg	cgg	agg	aag	432	
Leu	Ala	Gln	Gly	Lys	Lys	Gln	Arg	Leu	Ser	Lys	Lys	Leu	Arg	Arg	Lys		
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tta	cag	atg	tgg	ctg	tgg	tcg	cag	aca	ttc	tgc	ccc	gtg	ctg	tac	gcg	480	
Leu	Gln	Met	Trp	Leu	Trp	Ser	Gln	Thr	Phe	Cys	Pro	Val	Leu	Tyr	Ala		
	145				150					155					160		
tgg	aac	gac	ctg	ggc	agc	cgc	ttt	tgg	ccg	cgc	tac	gtg	aag	gtg	ggc	528	
Trp	Asn	Asp	Leu	Gly	Ser	Arg	Phe	Trp	Pro	Arg	Tyr	Val	Lys	Val	Gly		
			165					170						175			
agc	tgc	ttc	agt	aag	cgc	tcg	tgc	tcc	gtg	ccc	gag	ggc	atg	gtg	tgc	576	
Ser	Cys	Phe	Ser	Lys	Arg	Ser	Cys	Ser	Val	Pro	Glu	Gly	Met	Val	Cys		
			180					185					190				
aag	ccg	tcc	aag	tcc	gtg	cac	ctc	acg	gtg	ctg	cgg	tgg	cgc	tgt	cag	624	
Lys	Pro	Ser	Lys	Ser	Val	His	Leu	Thr	Val	Leu	Arg	Trp	Arg	Cys	Gln		
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cgg	cgc	ggg	ggc	cag	cgc	tgc	ggc	tgg	att	ccc	atc	cag	tac	ccc	atc	672	
Arg	Arg	Gly	Gly	Gln	Arg	Cys	Gly	Trp	Ile	Pro	Ile	Gln	Tyr	Pro	Ile		
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att	tcc	gag	tgc	aag	tgc	tcg	tgc	tag								699	
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35 40 45
His Pro Asp Pro Ile Phe Asp Pro Lys Glu Lys Asp Leu Asn Glu Thr
50 55 60
Leu Leu Arg Ser Leu Leu Gly Gly His Tyr Asp Pro Gly Phe Met Ala
65 70 75 80
Thr Ser Pro Pro Glu Asp Arg Pro Gly Gly Gly Gly Ala Ala Gly
85 90 95
Gly Ala Glu Asp Leu Ala Glu Leu Asp Gln Leu Leu Arg Gln Arg Pro
100 105 110
Ser Gly Ala Met Pro Ser Glu Ile Lys Gly Leu Glu Phe Ser Glu Gly
115 120 125
Leu Ala Gln Gly Lys Lys Gln Arg Leu Ser Lys Lys Leu Arg Arg Lys
130 135 140
Leu Gln Met Trp Leu Trp Ser Gln Thr Phe Cys Pro Val Leu Tyr Ala
145 150 155 160
Trp Asn Asp Leu Gly Ser Arg Phe Trp Pro Arg Tyr Val Lys Val Gly
165 170 175
Ser Cys Phe Ser Lys Arg Ser Cys Ser Val Pro Glu Gly Met Val Cys
180 185 190
Lys Pro Ser Lys Ser Val His Leu Thr Val Leu Arg Trp Arg Cys Gln
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Arg Arg Gly Gly Gln Arg Cys Gly Trp Ile Pro Ile Gln Tyr Pro Ile
210 215 220
Ile Ser Glu Cys Lys Cys Ser Cys
225 230

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<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

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<220>
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<210> 5
<211> 18

<212> DNA
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<220>
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18

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Gln Met Trp Leu Trp Ser
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<210> 8
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<400> 8
Glu Cys Lys Cys Ser Cys
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<220>
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<223> R = A or G

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<223> N = i - inosine

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 <221> modified_base
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 <223> Y = C or T

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<210> 10
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 Val Leu Gly Leu Arg Ala Thr Pro Ala Gly Gly Gln His Tyr Leu His
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 Ile Arg Pro Ala Pro Ser Asp Asn Leu Pro Leu Val Asp Leu Ile Glu
 35 40 45
 His Pro Asp Pro Ile Phe Asp Pro Lys Glu Lys Asp Leu Asn Glu Thr
 50 55 60
 Leu Leu Arg Ser Leu Leu Gly Gly His Tyr Asp Pro Gly Phe Met Ala
 65 70 75 80
 Thr Ser Pro Pro Glu Asp Arg Pro Gly Gly Gly Gly Ala Ala Gly
 85 90 95
 Gly Ala Glu Asp Leu Ala Glu Leu Asp Gln Leu Leu Arg Gln Arg Pro
 100 105 110
 Ser Gly Ala Met Pro Ser Glu Ile Lys Gly Leu Glu Phe Ser Glu Gly
 115 120 125
 Leu Ala Gln Gly Leu Gln Met Trp Leu Trp Ser Gln Thr Phe Cys Pro
 130 135 140
 Val Leu Tyr Ala Trp Asn Asp Leu Gly Ser Arg Phe Trp Pro Arg Tyr
 145 150 155 160
 Val Lys Val Gly Ser Cys Phe Ser Lys Arg Ser Cys Ser Val Pro Glu
 165 170 175
 Gly Met Val Cys Lys Pro Ser Lys Ser Val His Leu Thr Val Leu Arg
 180 185 190
 Trp Arg Cys Gln Arg Arg Gly Gly Gln Arg Cys Gly Trp Ile Pro Ile
 195 200 205
 Gln Tyr Pro Ile Ile Ser Glu Cys Lys Cys Ser Cys
 210 215 220